



SEQUENCE LISTING

<110> Chatfield, Steven N
Dougan, Gordon
Sydenham, Mark

<120> Vaccines Containing Attenuated Bacteria

<130> KC01003US

<140> US 09/591,447

<141> 2001-06-09

<150> UK 9726233.1

<151> 1997-12-11

<160> 4

<170> MS-DOS

<210> 1

<211> 1287

<212> DNA

<213> Salmonella typhimurium

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ctgcagatgg gtcagaagat gggggtgaag atcacggatg agcagttgga tcagccatca
300

gccaacatcg ccaaacaaaa caatatgacg atggatcaga tgcgcagccg tctggcttac
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gatgggctga actattcaac ctaccgtaac cagattcgta aagagatgat tatctctgaa
420

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TECH CENTER 1600/2900

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540

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600

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720

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1140

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<212> PRT

<213> Salmonella typhimurium

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Val Lys Leu Asn Ala Gly Gln Ala Gly Gln Gln Leu Pro Asp Asp Ala
 50 55 60

Thr Leu Arg His Gln Ile Leu Glu Arg Leu Ile Met Asp Gln Ile Ile
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Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Thr Asp Glu Gln Leu
 85 90 95

Asp Gln Pro Ser Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Met Asp
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Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Ser Thr Tyr
 115 120 125

Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn
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Glu Val Arg Arg Arg Ile Thr Val Leu Pro Gln Glu Val Asp Ala Leu
 145 150 155 160

Ala Lys Gln Ile Gly Thr Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu
 165 170 175

Ser His Ile Leu Ile Ala Leu Pro Glu Asn Pro Thr Ser Glu Gln Val
 180 185 190

Asn Asp Ala Gln Arg Gln Ala Glu Ser Ile Val Glu Glu Ala Arg Asn
 195 200 205

Gly Ala Asp Phe Gly Lys Leu Ala Ile Thr Tyr Ser Ala Asp Gln Gln
 210 215 220

Ala Leu Lys Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro

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Gly Ile Phe Ala	Gln Ala Leu Ser Thr	Ala Lys Lys Gly Asp	Ile Val			
	245	250	255			
Gly Pro Ile Arg	Ser Gly Val Gly	Phe His Ile Leu Lys	Val Asn Asp			
	260	265	270			
Leu Arg Gly Gln	Ser Gln Ser Ile	Ser Val Thr Glu	Val His Ala Arg			
	275	280	285			
His Ile Leu Leu	Lys Pro Ser Pro	Ile Met Asn Asp	Gln Gln Ala Arg			
	290	295	300			
Leu Lys Leu Glu	Glu Ile Ala Ala	Asp Ile Lys Ser	Gly Lys Thr Thr			
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Phe Ala Ala Ala	Ala Lys Glu Tyr	Ser Gln Asp Pro	Gly Ser Ala Asn			
	325	330	335			
Gln Gly Gly Asp	Leu Gly Trp Ala	Thr Pro Asp Ile	Phe Asp Pro Ala			
	340	345	350			
Phe Arg Asp Ala	Leu Thr Lys Leu	His Lys Gly Gln	Ile Ser Ala Pro			
	355	360	365			
Val His Ser Ser	Phe Gly Trp His	Leu Ile Glu Leu	Leu Asp Thr Arg			
	370	375	380			
Lys Val Asp Lys	Thr Asp Ala Ala	Gln Lys Asp Arg	Ala Tyr Arg Met			
	385	390	395			400
Leu Met Asn Arg	Lys Phe Ser Glu	Glu Ala Ala Thr	Trp Met Gln Glu			
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<210> 3

<211> 1287

<212> DNA

<213> Escherichia coli

<400> 3

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120

gacgttgatg gattaatgca gtcggtaaaa ctgaacgctg ctcaggcaag gcagcaactt
180

cctgatgacg cgacgctgcg ccaccaaatac atggaacgtt tgatcatgga tcaaatcatt
240

ctgcagatgg ggcagaaaat gggagtgaac atctccgatg agcagctgga tcaggcgatt
300

gctaacatcg cgaaacagaa caacatgacg ctggatcaga tgcgcagccg tctggcttac
360

gatggactga actacaacac ctatcgtaac cagatccgca aagagatgat tatctctgaa
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480

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540

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gccattgtcg atcaggcgcg taacggcgct gatttcggta agctggcgat tgctcattct
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gccgaccagc aggcgctgaa cggcggccag atgggctggg gccgtattca ggagttgccc
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gggatcttcg cccaggcatt aagcaccgcg aagaaaggcg acattgttgg cccgattcgt
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tcggtgaccg aagttcatgc tcgcatatt ctgctgaaac cgtcgccgat catgactgac
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960

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1200

ctgatgaacc gtaagttctc ggaagaagca gcaagctgga tgcaggaaca acgtgccagc
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gcctacgtta aaatcctgag caactaa
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<210> 4

<211> 428

<212> PRT

<213> Escherichia coli

<400> 4

Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn
1 5 10 15

Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val
20 25 30

Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
35 40 45

Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala
50 55 60

Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile
65 70 75 80

Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu
85 90 95

Asp Gln Ala Ile Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Leu Asp
100 105 110

Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Asn Thr Tyr
115 120 125

Arg	Asn	Gln	Ile	Arg	Lys	Glu	Met	Ile	Ile	Ser	Glu	Val	Arg	Asn	Asn
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Ala	Gln	Gln	Val	Gly	Asn	Gln	Asn	Asp	Ala	Ser	Thr	Glu	Leu	Asn	Leu
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Ser	His	Ile	Leu	Ile	Pro	Leu	Pro	Glu	Asn	Pro	Thr	Ser	Asp	Gln	Val
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Asn	Glu	Ala	Glu	Ser	Gln	Ala	Arg	Ala	Ile	Val	Asp	Gln	Ala	Arg	Asn
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Gly	Ile	Phe	Ala	Gln	Ala	Leu	Ser	Thr	Ala	Lys	Lys	Gly	Asp	Ile	Val
				245					250					255	
Gly	Pro	Ile	Arg	Ser	Gly	Val	Gly	Phe	His	Ile	Leu	Lys	Val	Asn	Asp
			260					265					270		
Leu	Arg	Gly	Glu	Ser	Lys	Asn	Ile	Ser	Val	Thr	Glu	Val	His	Ala	Arg
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His	Ile	Leu	Leu	Lys	Pro	Ser	Pro	Ile	Met	Thr	Asp	Glu	Gln	Ala	Arg
	290					295					300				
Val	Lys	Leu	Glu	Gln	Ile	Ala	Ala	Asp	Ile	Glu	Ser	Gly	Lys	Thr	Thr
305					310					315					320
Phe	Ala	Ala	Ala	Thr	Lys	Glu	Phe	Ser	Gln	Asp	Pro	Val	Ser	Ala	Asn
				325					330					335	
Gln	Gly	Gly	Asp	Leu	Gly	Trp	Ala	Thr	Pro	Asp	Ile	Phe	Asp	Pro	Ala
			340					345					350		
Phe	Arg	Asp	Ala	Leu	Thr	Arg	Leu	Asn	Lys	Gly	Gln	Met	Ser	Ala	Pro
		355					360					365			
Val	His	Ser	Ser	Phe	Gly	Trp	His	Leu	Ile	Glu	Leu	Leu	Asp	Thr	Arg
	370					375					380				

Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
 385 390 395 400

Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu
 405 410 415

A1
Cond

Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn
 420 425
